

sequence-listing Tobin Sugano.ST25
SEQUENCE LISTING

<110> Tobin, Elaine

Tobin, Elaine M

Sugano, Shoji

<120> Regulation of Circadian Rhythm and Flowering

<130> 13054.0200/UC99-253-2

<140> 09/359,026

<141> 1999-07-22

<150> 60/094,032

<151> 1998-07-14

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 1080

<212> DNA

<213> Arabidopsis thaliana

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<400> 1

gtcgaccac gggtcggaga agaaaaccc agattttctc gtctctctaa tttctttct
60

ctctcaagct tctcagaaag tctgacactt tcgagaatct aatctccaaa tttctttgtct 1
20

ttttggagaa ggaatogaat tatgtacaag gaacgtagtg gaggaggtgg tgggtgggtca 1
30

tcgagatcag agatccctgg tggagctatt gatcggaac gaatcaacga tgcactcaat 2
40

aagaaaactag agaaatcttc aacttcacc accacatcta ggggtttctc tctaaagac 2
00

aaagatccct tttctttcac atctactaaa actcagcttc ctgatgtgga atcggaact 3
60

gatagtgaag ggtctgatgt gagggtgatg gagggtgatg atcgtctgtg gatctcttg 4
20

ttttgtaatt tgagagggaa tgattcttc tgtgaagtct atgaagatta tattcaagat 4
30

gatttcaatc tttgtggttt aagtgggcaa gtccttact atgattatgc acttgatctc 5
40

atcttagatg ttgatcttc caacagtga atgtttactg atgaacagca tgaaatggtg 6
00

gaatcagctg ctgagatgct atatggtctt attcatgttc gttacatttc gactactaaa 6
60

ggaatggctg caatgactga gaagtacaag aactgtgatt tcgggagatg ccgagagtt 7
20

ttctgttgog gtcagtcttg tcttcagtt ggacaatccg atatcccgag atcgagtact 7
40

gtgaagatat actgacctaa atcgaggat atatcttacc cgggatctaa attccaagga 8
40

aatattgatg gagcgtactt tggaaccaca tctctcact tgttcttgat gacttacggg 9
20

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aacttaaagg cgcagaagcc tactcaaagg tatgtcccaa aaatctttgg ctccaaggta 9
60
cacaaaccat gatactagtg ctctgcattc tcaatgggtga tacatttagt ggctctgtaa 10
30
ttgcatacgg atgagcaact gaaacgatag ctgggggtgac tggagcatac atcaaccatt 10
80

<110> 2

<111> 276

<112> PRT

<113> Arabidopsis thaliana

<400> 2

Met Tyr Lys Glu Arg Ser Gly Gly Gly Gly Gly Gly Ser Ser Arg Ser
1 5 10 15

Glu Ile Leu Gly Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu
20 25 30

Asn Lys Lys Leu Glu Lys Ser Ser Thr Ser Thr Thr Thr Ser Arg Val
35 40 45

Phe Ser Ser Lys Asp Lys Asp Pro Phe Ser Phe Thr Ser Thr Lys Thr
50 55 60

Gln Leu Pro Asp Val Glu Ser Glu Thr Asp Ser Glu Gly Ser Asp Val
65 70 75 80

Ser Gly Ser Glu Gly Asp Asp Thr Ser Trp Ile Ser Trp Phe Cys Asn
85 90 95

Leu Arg Gly Asn Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln
100 105 110

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Asp Asp Phe Asn Leu Cys Gly Leu Ser Gly Gln Val Pro Tyr Tyr Asp
115 120 125

Tyr Ala Leu Asp Leu Ile Leu Asp Val Asp Ala Ser Asn Ser Glu Met
130 135 140

Phe Thr Asp Glu Gln His Glu Met Val Glu Ser Ala Ala Glu Met Leu
145 150 155 160

Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys Gly Met Ala
165 170 175

Ala Met Thr Glu Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg
180 185 190

Val Phe Cys Cys Gly Gln Ser Cys Leu Pro Val Gly Gln Ser Asp Ile
195 200 205

Pro Arg Ser Ser Thr Val Lys Ile Tyr Cys Pro Lys Cys Glu Asp Ile
210 215 220

Ser Tyr Pro Arg Ser Lys Phe Gln Gly Asn Ile Asp Gly Ala Tyr Phe
225 230 235 240

Gly Thr Thr Phe Pro His Leu Phe Leu Met Thr Tyr Gly Asn Leu Lys
245 250 255

Pro Gln Lys Pro Thr Gln Ser Tyr Val Pro Lys Ile Phe Gly Phe Lys
260 265 270

Val His Lys Pro
275

<210> 3

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<211> 32

<212> PRT

<213> Unknown

<220>

<223> potential metal-binding motif

<220>

<221> MISC_FEATURE

<222> (3)..(28)

<223> X = any amino acid

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> X = any amino acid

<400> 3

Cys	Pro	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10						15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Pro	Xaa	Cys
			20					25					30		

<210> 4

<211> 5

<212> PRT

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<213> Unknown

<220>

<223> conserved autophosphorylation site

<400> 4

Ser Ser Ser Glu Glu
1 5

<210> 5

<211> 6

<212> PRT

<213> Unknown

<220>

<223> CK2 recognition phosphorylation site

<400> 5

Ser Gly Ser Glu Gly Asp
1 5

<210> 6

<211> 5

<212> PRT

<213> Unknown

<220>

<223> CK2 recognition phosphorylation site

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<400> 6

Ser Glu Gly Asp Asp
1 5

<210> 7

<211> 50

<212> DNA

<213> Unknown

<220>

<223> c-myc Bgl-II site

<400> 7

aattgagatc tcatggagca aaagcttata agcgaggagg acttgaacat
50

<210> 8

<211> 49

<212> DNA

<213> Unknown

<220>

<223> c-myc Bgl-II site

<400> 8

gtacatgttc aagtcctcct cgctgataag cttttgctcc atgagatct
40

<210> 9

<211> 24

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<212> DNA

<213> Artificial Sequence

<220>

<223> CKB3 primer

<400> 9

acaaggaacg tagtggagga ggtg

24

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> CKB3 primer

<400> 10

aacctagat gtggtggtgg aag

20

<210> 11

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Specific peptide substrate

sequence-listing Tobin_Sugano.ST25

<400> 11

Arg	Arg	Arg	Asp	Asp	Asp	Ser	Asp	Asp	Asp
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